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152 VVQRITVHVTRRPVLYFHIRW---

78 LGKFLSEHLVWLYGNYLKLKYLILSRHRKERREHVCEHCHSHGMGHDMNIEEKRIPAFLV 137

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Query Match
Best Local Similarity

12.7%;
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Matches

62;

Conservative

50;

Score 222.5; DB 1; Pred. No. 5.3e-10; 50; Mismatches 63;

Length Indels

335; 55;

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ed through and the EMBI and the EMBI e no restric s content is ge by and f/www.isb-sib	SEQUENCE FROM N.A. STRAIN-BRISTOL N2; MEDLINE-94150718; PubMed-7906398; Wilson R., Ainscough R., Anderson K., Baynes C., Berks M. Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Craxcon M., Dear S., Du Z., Durbin R., Favello A., Frasel Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Johnston L., Jones M., Kershaw J., Kirsten J., Laisster I Latreille P., Lightning J., Lloyd C., Mortimore B., O'Ca. Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Sims M., Smaldon N., Smith M., Sonnhammer E., & Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaugh Waterson R., Watson A., Weinstock L., Wilkinson-Sproat J. "2.2 Mb of contiguous nucleotide sequence from chromosome elegans." Nature 368:32-38(1994). "1. SIMILARITY: TO POTASSIUM CHANNEL PROTEIN HAK-6.	SULT 1 TWK8_CAEEL STANDARD; PRT; 335 AA. p34410; 01-FEB-1994 (Rel. 28, Created) 01-FEB-1994 (Rel. 28, Last sequence update) 15-JUL-1998 (Rel. 36, Last annotation update) TWK-8 PROTEIN. TWK-8 OR F22B7.7. Caenorhabditis elegans. Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae; Peloderinae; Caenorhabditis. [1]	34 89 5.1 425 1 LIVM_ECOLI 35 89 5.1 614 1 YDNK_LACLC 36 88.5 5.0 484 1 ALLP_ECOLI 37 88 5.0 425 1 LIVM_SALTY 38 88 5.0 425 1 LIVM_SALTY 39 87.5 5.0 415 1 CSCB_ECOLI 40 87.5 5.0 470 1 CYCA_ECOLI 41 87.5 5.0 518 1 GITL_YEAST 42 87.5 5.0 624 1 PESL_HUMAN 43 87.5 5.0 624 1 PESL_HUMAN 44 87.5 5.0 624 1 CIKB_DROME 45 86.5 4.9 459 1 Y226_MYCGE ALIGNMENTS ALIGNMENTS
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P40310; Q05721;
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SEQUENCE FROM N.A.
MEDLINE-96303826; PubMed-8723646;
mard J.D., Lukas W., Shafaatian R.,
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Lesage F., Guillemare E., Fink M., Duprat F., Lazdunski Romey G., Barhanin J.;
Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The S. cerevisiae outwardly-rectifying potassium channel identifies a new family of channels with duplicated pore ecept. Channels 4:51-62(1996).
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Goldstein S.A.N.;
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Eukaryota; Fungi; Ascomycota; Saccharomycetes;
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Sequence and function analysis of a 9.
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                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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                                                                             the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
      SEQUENCE
                                                                 EMBL; U40959;
                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                      WORMPEP;
                                                                                                                                                         Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                           Caenorhabditis elegans
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TRANSMEM 72
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107 127 POTENTIAL.

138 158 POTENTIAL.

188 208 POTENTIAL.

228 AA; 25625 MW; 0822E836
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33; Mismatches
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2.7e-06;
71;
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                                                                                                                                                                                                                             Rhabditida; Rhabditoidea;
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Query Match Best Local Similarity

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01-NOV-1997
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Sclence 273:1058-1073(1996).
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN
-1- SIMILARITY: STRONG, TO M.JANNASCHII MJ1357.
-1- SIMILARITY: TO EUKARYOTIC POTASSIUM CHANNEIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PUTATIVE POTASSIUM
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                                                                                                                                                                                                                                                                                                                                                                                                          non-profit institutions as long as its content is in no way and this statement is not removed. Usage by and for commercial requires a license agreement (See http://www.isb-sib.ch/announce/
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                                             Score 121; DE
Pred. No. 0.02
25; Mismatches
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7CC082675F96B06A CRC64;
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D31069; P94716; P94717;

01-JUL-1993 (Rel. 26, C

01-JUL-1993 (Rel. 26, L

01-NOV-1997 (Rel. 35, L
                                                                                                                                                                                                                                                                                                                      SEQUENCE
STRAIN-K1
                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97426617; PubMed=9278503;

MEDLINE=97426617; PubMed=9278503;

Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burl Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew Riley M., Collado-Vides J., Glasner J.D., Goeden M.A., Rose D
                                    This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
                                                                                                                                                                  DNA
                                                                                                                                                                                                        Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y. Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;
                                                                                                                                                                              "A 570-kb DNA sequence of the Escherichia corresponding to the 28.0-40.1 min region
                                                                                                                                                                                                                                                                                                    MEDLINE=97251357; PubMed=9097039;
                                                                                                                                                                                                                                                                                                                                                              Science
                                                                                                                                                                                                                                                                                                                                                                                         Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=K12 / MG1655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Milkman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N. STRAIN-K12, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           proteins.
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MEDLINE=94224769; PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EQUENCE FROM N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     An Escherichia coli homologue of eukaryotic potassium
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                                                                                                            (POTENTIAL).
SIMILARITY:
                                                                                                                                      SUBCELLULAR LOCATION:
                                                                                                                                                   Res. 3:363-377(1996). FUNCTION: MAY PLAY A
                                                                                                                                                                                                                                                                                                                                                              complete genome sequence nce 277:1453-1474(1997).
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yhew G.F.,
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                                                               a collaboration -
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RESULT 6

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ID Y139_METJA

AC Q57603;

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Best Local :
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BL; U24195; AAB60079.1; ...

BL; U24197; AAB60087.1; ...

BL; U24199; AAB60087.1; ...

BL; U24199; AAB60103.1; ...

3L; U24200; AAB60111.1; ...

3L; U24201; AAB60111.1; ...

4L; U24202; AAB60119.1; ...

4L; U24203; AAB60119.1; ...

4L; U24204; AAB60119.1; ...

4L; U24204; AAB60119.1; ...

4L; U24204; AAB60119.1; ...

4L; U24205; AAB60119.1; ...

4L; U24206; AAB60119.1; ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                  DVKTVLAVSDSKNLNKIKMVHPD-----IILSPQLFGSEI 372
                                                                                                                                                                                                                                                -----RLGDNADVIPGDSNDSSV--LKKAGIDRCRAILALSDNDADNAFVVLSAKDMSS
                                                                                                                                                                                                                                                                                        ISLSTIGLG----DYVPGEGYNQKFRELYKIGI-TCYLLLGLI------AMLVV-----
                                                                                                                                                                                                                                                                                                                              KLVKGNNHTMHRKDHFIVCGHSILAINTILQLNQRGQNVTVISNLPEDDIKQLEQ----
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SMEM 22

MEM 87

SMEM 111

SMEM 141

SMEM 200

NNT 5

NNT 13

NNT 223

NNT 405
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(Rel. 35, Last sequence
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A -> T (IN STRAINS ECOR 52 AND E N -> K (IN STRAINS ECOR 4).

P -> S (IN STRAIN ECOR 4).

C -> O (IN STRAIN ECOR 4, ECOR 28, ECOR 31, ECOR 37, ECOR 46, E ECOR 52, ECOR 60 AND ECOR 71).

E -> K (IN STRAIN ECOR 46).

S -> U (IN STRAIN ECOR 46).

S -> U (IN STRAIN ECOR 46).
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Query Match
Best Local
                                         BACSU STANDARD; PRT; 393 AA.

NUPC_BACSU STANDARD; PRT; 393 AA.

P39141; 032288;

01-FEB-1995 (Rel. 31, Created)

30-MAY-2000 (Rel. 39, Last sequence update)

01-OCT-2000 (Rel. 40, Last annotation updat

01-OCT-2000 (Rel. 40, Last annotation updat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-JAL-1 / DSM 2661 / ATCC 43067;

STRAIN-JAL-1 / DSM 2661 / ATCC 43067;

MEDLINE=96337999; PubMed=8688087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,

"Compachii".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (S or send an email to license@isb-sib.ch).
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the European Bioinformatics Institute. There is
use by non-profit institutions as long as is
modified and this statement is not removed. Us
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Science 273:1058-1073(1996).
    Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a
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                       Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INTERPRO;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Methanococcus jannaschii
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                                                                                                                                                                                                                                                                                                                                                                                                      RPVLYFHIRWGFSKQVVAIV----------HAVLLGFVTVSCFFFIPAAVFSVL 206
                                                                                                                                                                                                                                                                              ESGVNPAINNFFDAFYFTTISITTVGYGDITP----KTDAGKLIIIFSVLFFISGLITSL
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                                                                                                                                                                                                                                                                                                                                                               ----VFYSKAFLGLRVINLLRILVLLRIIKLRKLEENQALINFLTLLTICFIASCLIWIV
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Firmicutes;
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11 31
72 92
126 146
157 17
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209 AA; 2
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21.7%;
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  Bacillus/Clostridium group;
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Pred.
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No. 0.
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tent is in no
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SEQUENCE FROM N.A. Bacillus/Staphylococcus

group; Bacillus

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Query Match
Best Local
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CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- SIMILARITY: BELONGS TO THE SLC28A FAMILY OF TRANSPORTERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yoshida K.-I., Fujimyra M., Yanai N., Fuji
"Cloning and sequencing of a 23-kb region
genome between the iol and hut operons.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saxild H.H., Andersen L.N., Hammer K.; "Dra-nupC-pdp operon of Bacillus subtilis: nucleotide sequence, induction by deoxyribonucleosides, and transcriptional regulation the deoR-encoded DeoR repressor protein.";

J. Bacteriol. 178:424-434(1996).
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PFAM; PF01773; Nucleoside_tra2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
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STRAIN-168 / BGSC1A1;
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                                                                                                                                                                                                                                                                                                                                                                                                                 Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBTILIST; BG10984; NUPC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97021444; PubMed=8867804;
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 194
                          292
                                                  140
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                                                                                                                                           CFFFIPAAVFSVLEDDWNFLESF--
                                                                                                                             VVTALVLNLFGGFIIASIINPYEVAKEEDMLRVE-EEEKQSIF---
                        VGIPWNEAVNAGSIMATKMVSNEFVAMTSLTQNGFH----FSGRTTAIVSVFLVSFANFS
                                                  IGIPFT----
                                                                         VVVAAMLIGFVAIIALINGIFN-----AVFGISFQGILGY
                                                                                                 RVLEASNYG-VSVLSNASGNWNWDFTSALFFASTVLSTTGYGHTVPLSDGGKAFCIIYSV 139
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D45912; BAA08338.1;
Z99124; CAB15977.1;
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3 23
32 52
87 107
168 188
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249 269
272 292
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372 392
16 16
16 16
30 30 $
30 AA; 42529 MW;
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                                                LLFLTAVVQRITVHVTRRPVLYFHIRWGFSKQVVAIVHAVLLGFVTVS
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                                                                                                                                                                              32;
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Pred. No. 1;
32; Mismatches
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SI -> RL (I
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I -> RL (IN REF. 1).
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C28677B5D3OAEOAC CRC64;
 -YFCFISLST:IGL 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fujita Y.;
gion of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (See http://www.isb-sib.
                                                                                                                                                                                                      DB 1.;
                                                                                                                                                                               ; 128
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                                                                                                                           EVLGEYILDGFKVA 248
                                                                                                                                                                                                       393;
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HLAEKTAKRTSYSRKEVLSYIFHHPALWVMMLLTMLIQTGNFSIQPLLALYVNELHGPVN 202

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RESULT 8
YUXJ_BACSU
ID YUXJ_BACSU
AC P40760;
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                                                                                          Matches
                                                                                                                                                                                                                                                          Hypothetical
TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oudega B., Koningsteijn G., Rodrigues L., Hilbert H., Duesterhoeft A., Pohl T.M., We "Analysis of the Bacillus subtilis genomosequence of a 62 kb region be".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1995
15-JUL-1998
15-DEC-1998
                                                                                                                                                                   TRANSMEM
SEQUENCE
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                                                                                                                                                                                                                                                                                                      EMBL; Z99120; CAB15137.1
EMBL; U11882; AAA64942.1
SUBTILIST; BG10976; YUXJ
                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Cloning, nucleotide sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                348
55
                              83
                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteriol. 176:7197-7205(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: INTEGRAL MEMBI SIMILARITY: STRONG, TO E.COLI YCEE.
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                                                            QSLAGSSCVRLVERHRSAWCFGFLVLGYL-----LYLVFGAVVFSSVELPYEDLLRQ
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                            KSSAGKTLGTLQMGQVSGSLFGPLLGGMLADRFGFTYTFFITSFVIFSSVLLVLFGVKEK 142
EL--RKLKRRFLEEHECLS-----EQQLEQFLGRVLEASNYGVSVLSNASGNWNWDFTS 106
                                                                                                                                                                                                                                                                                                                    Z93933; CAB07914.1; -.
Z99120; CAB15137.1; -.
U11882; AAA64942.1; -.
                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FROM N.A
                                                                                                                                                                              protein;
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                                                                                          Conservative
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                                                                                                                                                                    AA;
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POTENTIAL.
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Last annotation update)
PROTEIN IN KAPD-PBPD IN
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31758C0122231311 CRC64;
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                                                                                          Mismatches
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MBL outstation -
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15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV2.2
                                                                                                                                                                  the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CIKB_RAT
                                    PRINTS;
                                                                                                     EMBL; M77482;
                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neuron
                                                                                                                                                                                                                       between
                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through
                                                   PFAM; PF00520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      molecular cloning and characterization."; Neuron 8:473-481(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-92198655; PubMed-1550672;
Hwang P.M., Glatt C.E., Bredt D.S., Yellen G.,
"A novel K+ channel with unique localizations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
                   Ionic
                                                                   INTERPRO; IPR000636; -.
INTERPRO; IPR003091; -.
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EVERY THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL DOMAIN: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL TO SPECIFIC SUBCE
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TISSUE SPECIFICITY: IN THE BRAIN, THE GREATEST DENSITY OCCU
THE OLFACTORY BULLS, FOLLOWED BY THE CEREBRAL CORTEX, HIPPOC
AND CEREBELLUM. IN PERIPHERAL TISSUES IT IS MOST PROMINENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: THIS PRÓTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
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                                                                                                                                                                                                                                                                                                                                                                   WHOLE TONGUE EPITHELIUM AND CIRCUMVALLATE PAPILLAE.

DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS:
                                                                                                                                                                                                                                                                    SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DEL. CLASS. BELONGS TO SHAB POTASSIUM CHANNEL SUBFAMILY.
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                   channel;
                                    PR00169; KCHANNEL.
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Multigene family;
                                                  ion_trans; 1.
                 Transmembrane;
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               Ion
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Phosphorylation
               transport;
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                 Voltage-gated
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mammalian brain:
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                   channel;
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RESULT 10
AG22_HUMAN STANDARD; PRT; 363 AA.
ID AG22_HUMAN STANDARD; PRT; 363 AA.
AC P50052; Q13016;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE TYPE-2 ANGIOTENSIN II RECEPTOR (AT2).
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DOMAIN
                     Chassagne C., Beatty B.G., Meloche S.;
"Assignment of the human angiotensin II type 2 receptor gene to chromosome Xq22-q23 by fluorescence in situ hybridization. Genomics 25:601-603(1995).
SEQUENCE FROM N.A
                                                                      MEDLINE=95309939; PubMed=7790004;
                                                                                   TISSUE=PLACENTA;
                                                                                             SEQUENCE FROM N.A.
                                                                                                                      Biochem.
                                                                                                                                angiotensin II receptor.
                                                                                                                                                          Martin M.M., Elton T.
                                                                                                                                                                                TISSUE-LIVER;
                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                   Mammalia;
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                                                                                                                     Biophys.
                                                                                                                                                                                                                   Eutheria;
                                                                                                                                                                                                                                Metazoa;
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POLY-SER.
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CYTOPLASMIC (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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                                        (AGTR2)
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Submitted (JUN-1995) to the EMBL/GenBank/DBJ ditabases.
Submitted (JUN-1995) to the EMBL/GenBank/DBJ ditabases.
-i- FUNCTION: RECEPTOR FOR ANGIOTENSIN II. MAY HAVE A ROLE IN CELL
MORPHOGENESIS AND RELATED EVENTS IN GROWTH AND DEVELOPMENT.
-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDILINE-5091796; PubMed=7999093;
Martin M.M., Su B., Elton T.S.;
Molecular cloning of the human angiotensin II type
Biochem. Biophys. Res. Commun. 205:645-651(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=94242007; PubMed=8185599; Tsuzuki S., Ichiki T., Nakakubo H., Kitar Shirai H., Inagami T.; "Molecular cloning and expression of the "Molecular cloning and expression of angiotensin II type 2 receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Koike G., Horiuchi M., Yamada T., Szpirer C., Jacob H.J., I "Human type 2 angiotensin II receptor gene: Closed, mapped chromosome, and its mRNA is expressed in the human lung."; Biochem. Biophys. Res. Commun. 203:1842-1850(1994).
                                                                                                                                               HSSP;
                                                                                                                                                                EMBL;
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                                                                                                                                                                                                                                                                                                                              modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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TISSUE-BLOOD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Molecular characterization and chromosome localization of a human angiotensin II AT2 receptor gene highly expressed in fetal tissues."; Recept. Channels 2:271-280(1994).
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MEDLINE-95236034;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=95236034; PubMed=7719706; Lazard D., Briend-Sutren M.M., Villageois P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE SPECIFICITY: IN ADULT, HIGHLY EXPRESSED IN MYOMETRIUM WITH LOWER LEVELS IN ADRENAL GLAND AND FALLOPIAN TUBE. VERY HIGHLY EXPRESSED IN FETAL KIDNEY AND INTESTINE.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                European
                                                                                                                                                              U20860; AAA85851.1;
L34579; AAA89990.1;
U10273; AAA61794.1;
U15592; AAA50762.1;
U16597; AAA67753.1;
U16597; AAA86700.1;
U27478; AAA84900.1;
X87723; CAA61022.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                 P34996;
GCR_1057;
GCR_1245;
GCR_1876;
GCR_2011;
GCR_2027;
GCR_2031;
GCR_2056;
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pean Bioinformatics Institute.
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P15387;
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Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                     01-APR-1990 (Rel. 14, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV2.1
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INTERPRO;
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E; PS00237;
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00001; 7tm_1; 1.
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G_PROTEIN_RECEP_F1_2;
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20.9%;
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CW -> WC (IN REF. 5).
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Pred. No. 2.3;
40; Mismatches
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EXTRACELLULAR (POTENTIAL).
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3 (POTENTIAL)
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Craniata; Ver
Sciurognathi;
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(IN REF. 4).
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D (GLCNAC. . .)
D (GLCNAC. . .)
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Vertebrata; Euteleostomi;
hi; Muridae; Murinae; Rat
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Nature 340:642-645(1989).
                                                                                                                                                                                                                                                                                                                                        MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (FEB-1990)
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SEQUENCE FROM
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DOMAIN: THE TAIL MAY BE IMPORTANT IN MODULATION OF TARGETING OF THE CHANNEL
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TISSUE SPECIFICITY: IN THE BRAIN, THE GREATEST DENSITY OCCURS
THE CEREBRAL CORTEX, FOLLOWED BY THE HIPPOCAMPUS, CEREBELLUM,
OLFACTORY BULB. IN PERIPHERAL TISSUES IT IS MOST PROMINENT IN
RETINA AND KIDNEY. ALSO PRESENT IN CARDIAC MUSCLE TISSUE OF TH
ATRIUM AND VENTRICLE AND IN SKELETAL MUSCLE.
DOMAIN: THE SEGMENT-S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCORDANCE WITH THEIR ELECTROCHEMICAL WHITCH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
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EXTRACELLULAR (POTENTIAL).
SEGMENT S2 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
SEGMENT S3 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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y; Phosphorylation.
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RESULT 12
CIKA_HUMAN
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Q14721;
15-JUL-1998
15-JUL-1998
15-JUL-1998
Glycoprotein; Multigene
DOMAIN 1 182
TRANSMEM 183 204
DOMAIN 205 224
                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                the
                                                                                                                     EMBL; L02840; AAA36156.1; MIM; 600397; -.
                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ikeda S.R., Soler F.,
Submitted (JAN-1993) 1
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DOMAIN: THE SEGMENT S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           da S.R., Soler F., Zuhlke R.D., Joho R.H., Lewis D.L.;
mitted (JAN-1993) to the EMBL/GenBank/DDBJ databases.
FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
                                                                                                                                                                                                                ween the Swiss Institute of Bioinf
European Bioinformatics Institute.
                                                                                                                                                                                                                                                                     SIMILARITY: THI
CLASS. BELONGS
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DOMAIN: THE TAIL MAY BE
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                                                                                                                                                                                                                                                                                                 COMPARTMENTS.
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(Rel. 36, Last annotation update)
ED POTASSIUM CHANNEL PROTEIN KV2.1
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           orane; Ion transport; Voltage-gated family; Phosphorylation. CYTOPLASMIC (POTENTIAL). SEGMENT S1 (POTENTIAL).
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4 IS PROBABLY THE VOLTAGE-SENSOR
RIES OF POSITIVELY CHARGED AMINO
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SEQUENCE
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DOMAIN
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DOMAIN
                                                                                              SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE=FETAL;
MEDLINE-94092107; PubMed-8267573;
Nakajima M., Mukoyama M., Pratt R
"Cloning of cDNA and analysis of type 2 receptor.";
                                                                                                                                                                                           01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last seq
15-JUL-1998 (Rel. 36, Last ann
TYPE-2 ANGIOTENSIN II RECEPTOR
                                 MEDLINE-94122216; PubMed-8292631; Ichiki T., Herold C.L., Kambayashi Y., "Cloning of the cDNA and the genomic D
                                                             SEQUENCE FROM N.A. STRAIN-BALB/C;
                                                                                                                                                           Mus musculus (Mouse
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                AG22_MOUSE P35374;
                         "Cloning of the cDNA and type 2 receptor.";
                                                                                       Biochem.
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                                                                                      Biophys. Res.
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21.7%;
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                  1189:247-250(1994)
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EXTRACELLULAR (POTENTIAL).
SEGMENT S4 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
SEGMENT S5 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
SEGMENT S6 (POTENTIAL).
SEGMENT S6 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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Sciurognathi;
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360DEB3E45731EDA CRC64;
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thi; Muridae; Murinae; Mus
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INTERPRO; IPRO00147; -.
INTERPRO; IPRO00248; -.
INTERPRO; IPRO00276; -.
PFAM; PF00001; 7tm_1; 1.
PRINTS; PR00237; GFCRRHODOPSN.
PRINTS; PR00237; ANGIOTENSNIR.
PRINTS; PR00536; ANGIOTENSN2R.
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CARBOHYD
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EMBL;
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GCRDB; GCR_1007; -.
GCRDB; GCR_1010; -.
MGD; MGI:87966; AGTR2.
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; U004828; AAC52128.1;
; U00766; AAC04933.1;
; L32840; AAB49539.1; i
; U11073; AAA82184.1;
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71 71 80 102 1149 1140 1160 1179 2208 2278 3313 3313 3313 3363

3 (POTENTIAL).
CYTOPLASMIC (FOTENTIAL).

(POTENTIAL).

EXTRACELLULAR (POTENTIAL) 3 (POTENTIAL).

CYTOPLASMIC
2 (POTENTIAL

(POTENTIAL).

(POTENTIAL) (POTENTIAL) Transmembrane;

EXTRACELLULAR

(POTENTIAL) Glycoprotein;

EXTRACELLULAR (POTENTIAL).

5 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

6 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

7 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

(POTENTIAL).
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                              -i- FUNCTION: RECEPTOR FOR ANGIOTENSIN II. MAY HAVE MORPHOGENESIS AND RELATED EVENTS IN GROWTH AND D. -i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. -i- TISSUE SPECIFICITY: ABUNDANT IN FETUS, LOWER LEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The growth-dependent expression of angiotensin II type 2
regulated by transcription factors interferon regulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Horiuchi M., Koike
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=BALB/C; TISSUE=LIVER; MEDLINE=95378283; PubMed=765
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MOD_RES
SEQUENCE
       Inagami
Guo D.F.
                                                                     Dzau V.J., Jacob H.J., Dzau V.J., Jacob H.J., end "Cloning, characterization, and "Cloning, characterization, and angiotensin II receptor gene.", englishmentension 26:998-1002(1995).
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30-MAY-2000 (Rel. 3
TYPE-2 ANGIOTENSIN
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         Guo
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Dzau V.J.;
                                                                                                                                                                                                                                                                                    STRAIN-SPRAGUE-DAWLEY; TISSUE-FETAL; MEDLINE-94043302; PubMed-8227010;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                     STRAIN-FISCHER;
                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                            unique class
                                                                                                                                                                                                                                         "Expression cloning of type 2
                                     MEDLINE=95228708; PubMed=7713098;
                                                    SEQUENCE
                                                                                                                                      MEDLINE-96088876; PubMed-7490161;
Koike G., Winer E.S., Horiuchi M.,
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m. 268:24539-24542(1993).
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5; PubMed=7490161;
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       Score 94.5; D:
Pred. No. 2.7;
40; Mismatches
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Kambayashi
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PRINTS; PR00241; ANGIOTENSINR
PRINTS; PR00636; ANGIOTENSN2R
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INTERPRO; IPR000276; -.
PFAM; PF00001; 7tm_1; 1.
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-!- FUNCTION: RECEPTOR FOR ANGIOTENSIN II MAY HAMORPHOGENESIS AND RELATED EVENTS IN GROWTH AND ORPHOGENESIS AND ORPHOGENESI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ichiki T.;
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Ishii M., Murakami K., Miyazaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-SPRAGUE-DAWLEY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: INTEGRAL MEMBRAME PROTEIN.
TISSUE SPECIFICITY: ABUNDANT EXPRESSION IN FETAL TISSUES, 1
BRAIN, SKIN WOUND AND ATRETIC OVARIAN FOLLICLES.
DEVELOPMENTAL STAGE: ABUNDANT IN WHOLE FETUS BUT DECREASES
AFTER BIRTH. IN ADULTS IS HIGHLY EXPRESSED. IN THE ADRENAL,
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AAA86509.1; -.
BAA07833.1; -.
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G_PROTEIN_RECEP_F1_2; 1.
receptor; Transmembrane;
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MEDLINE-99299248; PubMed=10369879;

Coucke P.J., Van Hauwe P., Kelley P.M., Kunst H., Schatteman :

Van Velzen D., Meyers J., Ensink R.J., Verstreken M., Declau J.

Marres H., Kastury K., Bhasin S., McGuirt W.T., Smith R.J.H.,

Cremers C.W.R.J., Van de Heyning P., Willems P.J., Smith S.D.
                                                                                                                                                                                                                                                                                                                                                                                             "KCNQ4, a novel potassium channel expressed in cells, is mutated in dominant deafness."; Cell 96:437-446(1999).
                                                                                                                                                                                                                                "Mutations in the KCNQ4 gene are responsible deafness in four DFNA2 families."; Hum. Mol. Genet. 8:1321-1328(1999).
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El-Amraoui A., Marlin S., Petit C., Jentsch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND VARIANT DENA2 SER-285.
MEDLINE-99148276; PubMed-10025409;
Kubisch C., Schroeder B.C., Friedrich T., Luet
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15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KQT-LIKE
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                                                    OF THE HAIR CELL.

SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

TISSUE SPECIFICITY: EXPRESSED IN THE OUTER, BUT NOT THE INNI
SENSORY HAIR CELLS OF THE COCHLEA.

DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS
EVERY THIRD POSITION (BY SIMILARITY).

DISEASE: DEFECTS IN KCNQ4 ARE A CAUSE OF AUTOSOMAL DOMINANT
NONSYNDROMIC SENSORINEURAL DEAFNESS TYPE 2 (DFNA2).

SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECT
                                                                                                                                                                                                                    FUNCTION: MAY BE RESPONSIBLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 94.5;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----GNRFQQKLRSVFRVPIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -SCEVIAVIDLALPFATLLGF-TNSC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                   FOR
                                                                                                                                                                                                                   POTASSIUM IONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    695
produced through a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Luetjohann
ch T.J.;
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                                                                                                                                                                                                                                                                   for autosomal dominant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -GVSVLSNASGNWN
                                                        DELAYED RECTIFIER
                                                                                                                                                                                                                    AFTER
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                                                                                                                                                                                                                                                                                                                                                                                                                Multigene
TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTERPRO; IPR000636; INTERPRO; IPR003091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIM; 603537;
MIM; 600101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                         VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                         FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                  Ionic channel; Transmembrane; Ion transport; Voltage-gated
         257
                            257
                                                                 205
                                                                                   155
                                                                                                      167
                                                                                                                         104
                                                                                                                                             122
                                                                                                                                                              48
                                                                                                                                                                                                                                Local
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:: |: | | | | | |
                            YLAEKDANSDFSSYADSLWWGTITLTTIGYGDKTPHTWLGRVLAAGFALLGISFFALPAG
                                                                                                                                                             YEDLLRQELRKLKRRFLEEHECLSEQQLEQFLGRVLEASNYGVSVLSNAS----GNWNWD
                                                                                                                                                                                                    AGSSC-----
                                                                                                                        FTSALFFASTVLSTTGYGHTVPLSDGGKAFCIIYSVIGIPFTL-----LFLTAVVQ
                                                                                                                                           QE---HQEL----ANECL---LILEFVMIVVFGLEYIVRVWSAGCCCRYRGWQGR
                                                                                   RI----TVHVTRR----
                                                                                                      FRFA--
                                                                                                                                                                                 SGSACGQRSSAAHKRYRRLQNWYYNVLERPR-GWAFVYHV--FIFLLVFSCLVLSVLSTI
                                             PAAVFSVLEDDWNFLESFYFCFISLSTIGLGDYVPGEGYNQKFRELYK-IGITCYLL-LG
                                                                SMRFLQILRMVRMDRRGGTWKLLGSVVYAH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF105202;
AF105216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AF105212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF105209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AF105207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF1052
                                                                                                                                                                                                                      70;
                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                             PR00169;
                                                                                                                                                                                                                                                                                                                                                        family;
45
98
98
132
173
238
238
298
276
                                                                                                                                                                                                                                                                      695
                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                        321
                                                                                                                                                                                                                                                                                                          285
                                                                                                                                                                                                                                                                                                                                                                                                                                            ion_trans;
9; KCHANNEL.
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AAD14681.1;
AAD14681.1;
AAD14681.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                          Disease mutation;
                                                                                                                                                                                                                                                                                                                                                         118
152
193
258
318
276
                                                                                                                                                                                                                                                                                       321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14681.1;
14681.1;
                                                                                                                                                                                                  -----VRLVERHRSAWCFGFLVLGYLLYLVFGAVVFSSVELP
                                                                                                                                                                                                                                                                      77091 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14681.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4681.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4681.1;
                                                                                                                                                                                                                              5.4%;
21.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOINED.
                                                                                                                                                                                                                                                                           G -> C (IN DFNA2; LOSS OF I
SELECTIVITY OF THE PORE).
/FIId-VAR.008727.
G -> S (IN DFNA2).
/FIId-VAR.001547.
G -> S (IN DFNA2).
/FIId-VAR.008728.
         278
                                                                                                                                                                                                                               Score 94;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                  PVLYFHIRWGFSKQVVAIVHAVLLGF-VTVSCFFFI
                                                                                                                                                                                                                                                                                                                                                /FTId-VAR_008726
                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
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                                                                                                      RKPFCVIDFIVFVASVAVIAAGTQGNIFATSALR
                                                                                                                                                                                                                                                                    A58737BD845E1A3A CRC64;
                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                         S (IN
                                                                                                                                                                                                                                                                                                                                                                                                                         Deafness
                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                        ВВ
                                                                -SKELIT---AWYIGFLVLIFASFLV
                                                                                                                                                                                                                                                                                                                                                        DFNA2).
                                                                                                                                                                                                                      108;
                                                                                                                                                                                                                                        Length
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                                                                                                                                                                                                                                         695;
                                                                                                                                                                                                                                                                                                                                      POTASSIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                    channel;
                                                                                                                                                                                                                      98;
                                                                                                                                                                                                                     Gaps
                                                                                                                                                              103
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                                                                                                                                                                                                   47
                                                                                   198
                                                                                                                        154
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                                             256
                                                                256
                                                                                                      204
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Search completed: February 14, 2001, 03:43:05 Job time: 28254 sec